Molecular Classification of Breast Cancer: R01 CA96483
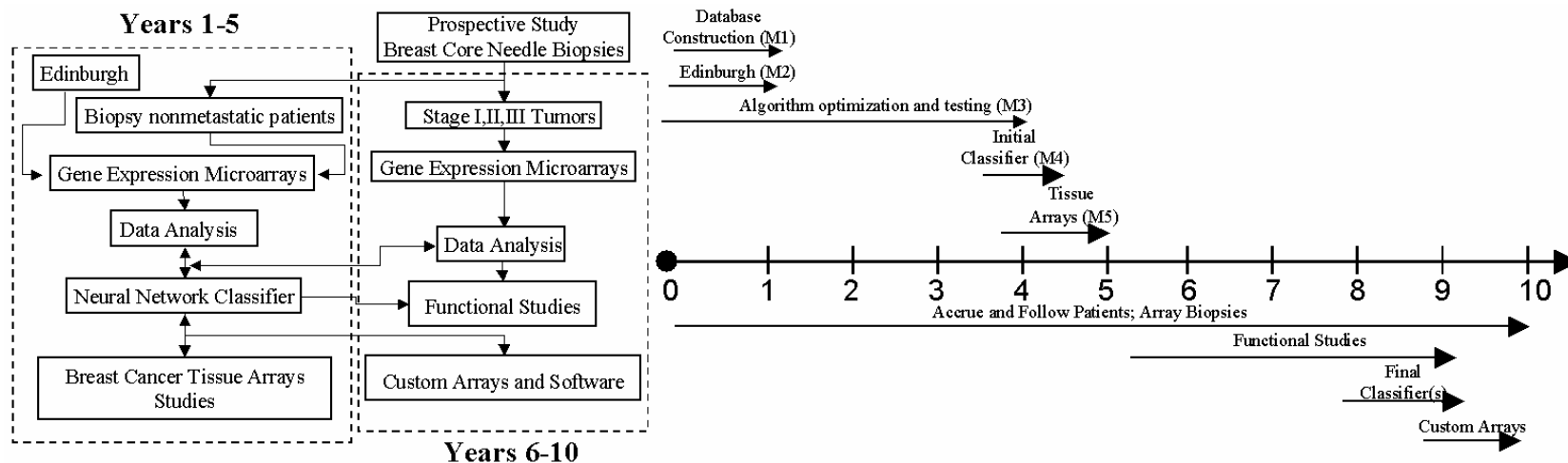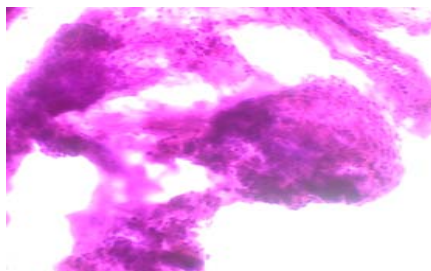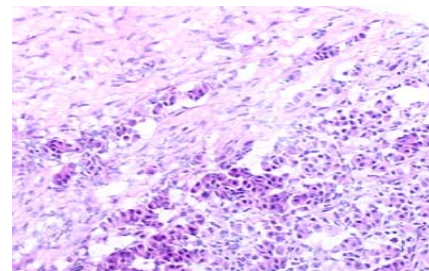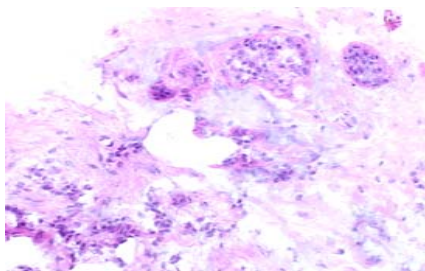
Project Overview

Tissue Processing
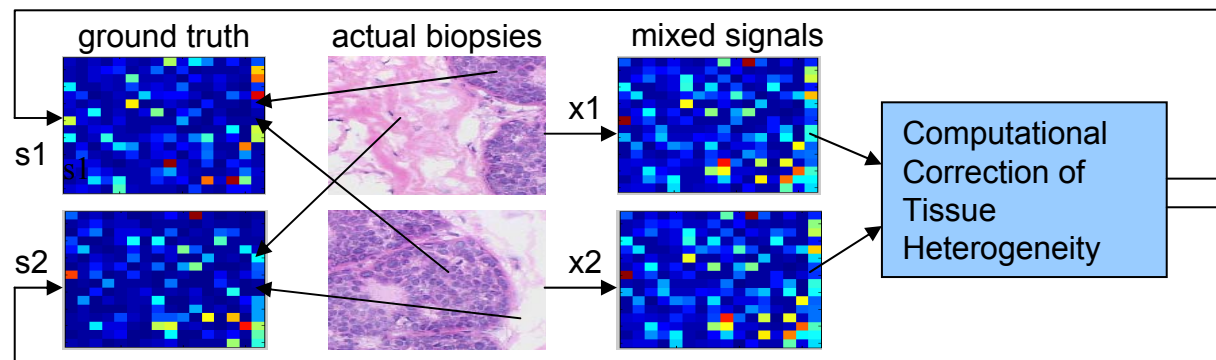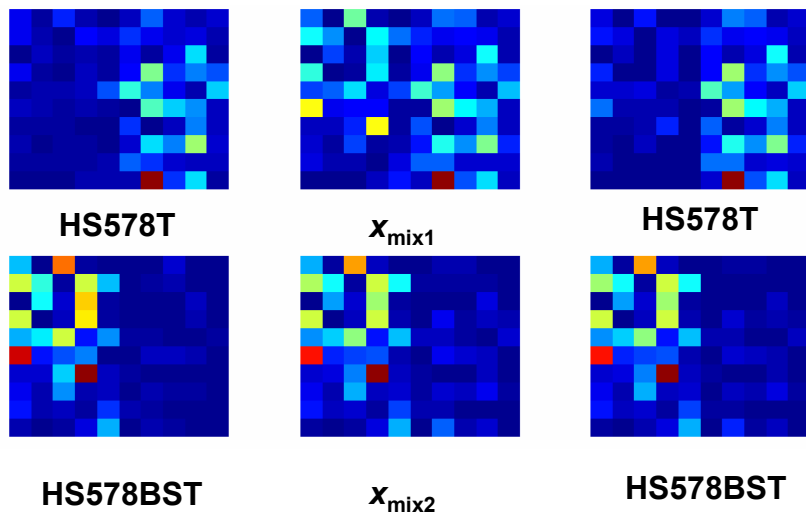

Unoptimized　　　　　　　　　　　Optimized

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Tissue Heterogeneity Correction (in silico)

ground truth   actual biopsies   mixed signals

s1   x1   Computational Correction of Tissue Heterogeneity
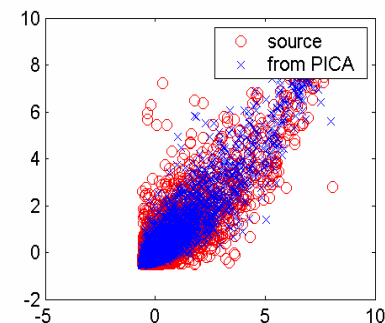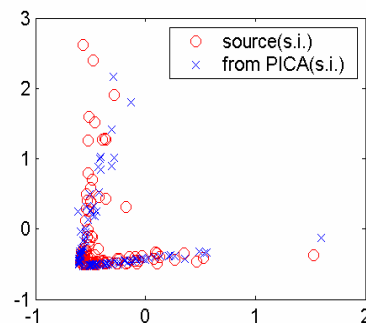
s2   x2

The task is to "blindly" recover the source signals ($s_{cancerous}(i)$, $s_{stromal}(i)$) from their observed mixtures ($x_{biopsy1}(i)$ and $x_{biopsy2}(i)$).

HS578T (breast cancer cell line) and HS578BST (fibroblast cell line from same patient).

HS578T x_{mix1} **HS578T**

HS578BST x_{mix2} **HS578BST**

$$x_{mix1} = 0.75 * s_{HS578T} + 0.25 * s_{HS578BST}$$

$$x_{mix2} = 0.25 * s_{HS578T} + 0.75 * s_{HS578BST}$$

Mixture observations
red = ground truth; blue = recovered sources

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